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1631

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Attorney Docket No. P20294

In re application of Akiko ITAI et al.

**Mail Stop Non-Fee**

Serial No. 09/700,708 (National Stage of PCT/JP98/02302)

Group Art Unit: 1631

Filed : November 24, 2000  
(I.A. Filed May 26, 1998)

Examiner: Michael Borin

For : METHOD FOR PREDICTING FUNCTIONS OF PROTEIN

**Mail Stop Non-Fee**

COMMISSIONER FOR PATENTS  
P.O. Box 1450  
Alexandria, Virginia 22313-1450

Sir:

Transmitted herewith is an Amendment under 37 C.F.R. 1.111 in the above-captioned application.

☐ Small Entity Status of this application under 37 C.F.R. 1.9 and 1.27 has been established by a previously filed statement.☐ A verified statement to establish small entity status under 37 C.F.R. 1.9 and 1.27 is enclosed.☒ A Request for Extension of Time.☐ No Additional Fee.☒ An article- The Ninth Workshop on Genome Informatics.

The fee has been calculated as shown below:

Claims After Amendment	No. Claims Previously Paid For	Present Extra	Small Entity		Other Than A Small Entity	
			Rate	Fee	Rate	Fee
Total Claims: 4	20	0	x 9=	\$	x 18=	\$0.00
Indep. Claims: 1	3	0	x 42=	\$	x 84=	\$0.00
Multiple Dependent Claims Presented			140=	\$	+280=	\$0.00
Extension Fees for three Months				\$		\$930.00
Total:				\$	Total:	\$930.00

\*If less than 20, write 20

\*\*If less than 3, write 3

☐ Please charge my Deposit Account No. 19-0089 in the amount of \$\_\_\_\_\_.☒ A Check in the amount of \$ 930.00 to cover the extension fee is included.☒ The U.S. Patent and Trademark Office is hereby authorized to charge payment of the following fees associated with this communication or credit any overpayment to Deposit Account No. 19-0089.☒ Any additional filing fees required under 37 C.F.R. 1.16.☒ Any patent application processing fees under 37 C.F.R. 1.17, including any required extension of time fees in any concurrent or future reply requiring a petition for extension of time for its timely submission (37 CFR 1.136)(a)(3).

Bruce H. Bernstein  
Reg No. 29,027

SEP 05 2003

PATENT &amp; TRADEMARK OFFICE

GIW '98



## The Ninth Workshop on Genome Informatics

December 10-11, 1998

Yebisu Garden Place, Tokyo, Japan

( <http://www.hgc.ims.u-tokyo.ac.jp/giw> )

Last Updated: January 6, 1998

Electronic Version of Genome Informatics Vol. 9 (1998)

The Ninth Workshop on Genome Informatics (GIW '98) is a forum for researchers, practitioners and users working on various aspects of Genome Informatics. The aim is to present recent research results (theory/practice), to demonstrate systems, and to explore directions for future research and new applications related to Genome Science.

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program.ps program.pdf program.txt
- List
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  - Full Papers
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- Information for Paper Presentation
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- Call for Papers
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- Commercial Exhibitions
- Registration (CLOSED: December 7, 1998)
- Hotel Reservation (CLOSED: November 10, 1998)
- Location
- Passport and Visa Requirements
- Genome Informatics Series

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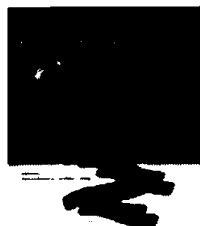
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GIW '98(The 9th Workshop on Genome Informatics)

Mail: giw@ims.u-tokyo.ac.jp



## Genome Informatics Vol. 9 (1998)

Presented at the Genome Informatics Workshop 1998  
December 10–11, 1998, Yebisu Garden Place, Tokyo, Japan

Published as: Miyano, S. and Takagi, T. (eds.) "Genome Informatics 1998"  
Universal Academy Press, Tokyo, 1998

Preface by Toshihisa Takagi

Program Committee

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### Full Talk Papers

#### Genomic Analysis of the Genes Encoding Ribosomal Proteins in Eight Eubacterial Species and *Saccharomyces cerevisiae*

Katsutoshi Fujita, Tomoya Baba, Katsumi Isono

Genome Informatics 9: 3–12 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

#### Construction of the *gyrB* Database for the Identification and Classification of Bacteria

Hiroaki Kasai, Kanako Watanabe, Elizabeth Gasteiger, Amos Bairoch, Katsumi Isono, Satoshi Yamamoto, Shigeaki Harayama

Genome Informatics 9: 13–21 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

#### Phylogenetic Invariants for Metazoan Mitochondrial Genome Evolution

David Sankoff, Mathieu Blanchette

Genome Informatics 9: 22–31 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

#### Systematic Prediction of Orthologous Units of Genes in the Complete Genomes

Hidemasa Bono, Susumu Goto, Wataru Fujibuchi, Hiroyuki Ogata, Minoru Kanehisa

Genome Informatics 9: 32–40 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

#### Comprehensive Sequence Analyses of 5' Flanking Regions of Primate Alu Elements

Yoshimi Toda, Rintaro Saito, Masaru Tomita

Genome Informatics 9: 41–48 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

#### Evidence of Limited Structural Organization in Globin Intron Sequences of Messenger RNA

Wayne Dawson, Kenji Yamamoto

Genome Informatics 9: 49–61 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

#### Identifying the Interaction between Genes and Gene Products Based on Frequently Seen Verbs in Medline Abstracts

Takeshi Sekimizu, Hyun S. Park, Jun'ichi Tsujii

Genome Informatics 9: 62–71 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

**Detecting Gene Symbols and Names in Biological Texts : A First Step toward Pertinent Information Extraction**

Denys Proux, François Rechenmann, Laurent Julliard, Violaine Pillet, Bernard Jacq  
Genome Informatics 9: 72-80 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

**Developing NLP Tools for Genome Informatics: An Information Extraction Perspective**

Teruyoshi Hishiki, Nigel Collier, Chikashi Nobata, Tomoko Okazaki-Ohta, Norihiro Ogata, Takeshi Sekimizu, Roland Steiner, Hyun S. Park, Jun'ichi Tsujii  
Genome Informatics 9: 81-90 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

**A Machine Learning Approach to Reducing the Work of Experts in Article Selection from Database: A Case Study for Regulatory Relations of *S. cerevisiae* Genes in MEDLINE**

Shin-ichi Usuzaka, Kim Lan Sim, Miyako Tanaka, Hiroshi Matsuno, Satoru Miyano  
Genome Informatics 9: 91-101 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

**Using Kleisli to Bring Out Features in BLASTP Results**

Jing Chen, Daphna Strauss, Limsoon Wong  
Genome Informatics 9: 102-111 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

**MUSCA: An Algorithm for Constrained Alignment of Multiple Data Sequences**

Laxmi Parida, Aris Floratos, Isidore Rigoutsos  
Genome Informatics 9: 112-119 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

**Improvement of the A\* Algorithm for Multiple Sequence Alignment**

Hirotsada Kobayashi, Hiroshi Imai  
Genome Informatics 9: 120-130 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

**Parallel Protein Information Analysis (PAPIA) System Running on a 64-Node PC Cluster**

Yutaka Akiyama, Kentaro Onizuka, Tamotsu Noguchi, Makoto Ando  
Genome Informatics 9: 131-140 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

**Finding Genetic Network from Experiments by Weighted Network Model**

Kiyoshi Noda, Ayumi Shinohara, Masayuki Takeda, Satoshi Matsumoto, Satoru Miyano, Satoru Kuhara

Genome Informatics 9: 141-150 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]

**A System for Identifying Genetic Networks from Gene Expression Patterns Produced by Gene Disruptions and Overexpressions**

Tatsuya Akutsu, Satoru Kuhara, Osamu Maruyama, Satoru Miyano

Genome Informatics 9: 151-160 (1998)

[Abstract] [Full-text HTML] [Full-text PDF]